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RAW SEQUENCE LISTING

DATE: 08/09/2004

PATENT APPLICATION: US/10/799,943

TIME: 09:35:03

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\08092004\J799943.raw

4 <110> APPLICANT: KADOWAKI, Takashi
 5 YAMAUCHI, Toshimasa
 6 NAGAI, Ryoza
 7 KAMON, Jyunji
 9 <120> TITLE OF INVENTION: ADIPONECTIN RECEPTOR AND GENE ENCODING
 10 THE SAME
 12 <130> FILE REFERENCE: ARV-002
 14 <140> CURRENT APPLICATION NUMBER: 10/799943
 15 <141> CURRENT FILING DATE: 2004-03-11
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07515
 18 <151> PRIOR FILING DATE: 2003-06-12
 20 <150> PRIOR APPLICATION NUMBER: JP 2002-383738
 21 <151> PRIOR FILING DATE: 2002-12-29
 23 <160> NUMBER OF SEQ ID NOS: 8
 25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1128
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)...(1125)
 36 <400> SEQUENCE: 1
 37 atg tct tcc cac aaa gga tct gtg gtg gca cag ggg aat ggg gct cct 48
 38 Met Ser Ser His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro
 39 1 5 10 15
 41 gcc agt aac agg gaa gct gac acg gtg gaa ctg gct gaa ctg gga ccc 96
 42 Ala Ser Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro
 43 20 25 30
 45 ctg cta gaa gag aag ggc aaa cgg gta atc gcc aac cca ccc aaa gct 144
 46 Leu Leu Glu Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala
 47 35 40 45
 49 gaa gaa gag caa aca tgc cca gtg ccc cag gaa gaa gag gag gag gtg 192
 50 Glu Glu Glu Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Val
 51 50 55 60
 53 cgg gta ctg aca ctt ccc ctg caa gcc cac cac gcc atg gag aag atg 240
 54 Arg Val Leu Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met
 55 65 70 75 80
 57 gaa gag ttt gtg tac aag gtc tgg gag gga cgt tgg agg gtc atc cca 288
 58 Glu Glu Phe Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro
 59 85 90 95
 61 tat gat gtg ctc cct gac tgg cta aag gac aac gac tat ctg cta cat 336
 62 Tyr Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His

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63	100	105	110	
65	ggt cat aga cct ccc atg ccc tcc ttt cgg gct tgc ttc aag agc atc	384		
66	Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile			
67	115 120 125			
69	ttc cgc att cat aca gaa act ggc aac atc tgg acc cat ctg ctt ggt	432		
70	Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly			
71	130 135 140			
73	ttc gtg ctg ttt ctc ttt ttg gga atc ttg acc atg ctc aga cca aat	480		
74	Phe Val Leu Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn			
75	145 150 155 160			
77	atg tac ttc atg gcc cct cta cag gag aag gtg gtt ttt ggg atg ttc	528		
78	Met Tyr Phe Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe			
79	165 170 175			
81	ttt ttg ggt gca gtg ctc tgc ctc agc ttc tcc tgg ctc ttt cac acc	576		
82	Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr			
83	180 185 190			
85	gtc tat tgt cat tca gag aaa gtc tct cgg act ttt tcc aaa ctg gac	624		
86	Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp			
87	195 200 205			
89	tat tca ggg att gct ctt cta att atg ggg agc ttt gtc ccc tgg ctc	672		
90	Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu			
91	210 215 220			
93	tat tat tcc ttc tac tgc tcc cca cag cca cgg ctc atc tac ctc tcc	720		
94	Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser			
95	225 230 235 240			
97	atc gtc tgt gtc ctg ggc att tct gcc atc att gtg gcg cag tgg gac	768		
98	Ile Val Cys Val Leu Gly Ile Ser Ala Ile Val Ala Gln Trp Asp			
99	245 250 255			
101	cgg ttt gcc act cct aag cac cgg cag aca aga gca ggc gtg ttc ctg	816		
102	Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu			
103	260 265 270			
105	gga ctt ggc ttg agt ggc gtc gtg ccc acc atg cac ttt act atc gct	864		
106	Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala			
107	275 280 285			
109	gag ggc ttt gtc aag gcc acc aca gtg ggc cag atg ggc tgg ttc ttc	912		
110	Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe			
111	290 295 300			
113	ctc atg gct gtg atg tac atc act gga gct ggc ctt tat gct gct cga	960		
114	Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg			
115	305 310 315 320			
117	att cct gag cgc ttc ttt cct gga aaa ttt gac ata tgg ttc cag tct	1008		
118	Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser			
119	325 330 335			
121	cat cag att ttc cat gtc ctg gtg gtg gca gca gcc ttt gtc cac ttc	1056		
122	His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe			
123	340 345 350			
125	tat gga gtc tcc aac ctt cag gaa ttc cgt tac ggc cta gaa ggc ggc	1104		
126	Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly			
127	355 360 365			

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129 tgt act gat gac acc ctt ctc tga                      1128
130 Cys Thr Asp Asp Thr Leu Leu
131      370                      375
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 375
136 <212> TYPE: PRT
137 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 2
140 Met Ser Ser His Lys Gly Ser Val Val Ala Gln Gly Asn Gly Ala Pro
141 1      5      10      15
142 Ala Ser Asn Arg Glu Ala Asp Thr Val Glu Leu Ala Glu Leu Gly Pro
143      20      25      30
144 Leu Leu Glu Lys Gly Lys Arg Val Ile Ala Asn Pro Pro Lys Ala
145      35      40      45
146 Glu Glu Glu Gln Thr Cys Pro Val Pro Gln Glu Glu Glu Glu Val
147      50      55      60
148 Arg Val Leu Thr Leu Pro Leu Gln Ala His His Ala Met Glu Lys Met
149 65      70      75      80
150 Glu Glu Phe Val Tyr Lys Val Trp Glu Gly Arg Trp Arg Val Ile Pro
151      85      90      95
152 Tyr Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp Tyr Leu Leu His
153      100     105     110
154 Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys Phe Lys Ser Ile
155      115     120     125
156 Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr His Leu Leu Gly
157      130     135     140
158 Phe Val Leu Phe Leu Phe Leu Gly Ile Leu Thr Met Leu Arg Pro Asn
159 145     150     155     160
160 Met Tyr Phe Met Ala Pro Leu Gln Glu Lys Val Val Phe Gly Met Phe
161      165     170     175
162 Phe Leu Gly Ala Val Leu Cys Leu Ser Phe Ser Trp Leu Phe His Thr
163      180     185     190
164 Val Tyr Cys His Ser Glu Lys Val Ser Arg Thr Phe Ser Lys Leu Asp
165      195     200     205
166 Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe Val Pro Trp Leu
167      210     215     220
168 Tyr Tyr Ser Phe Tyr Cys Ser Pro Gln Pro Arg Leu Ile Tyr Leu Ser
169 225     230     235     240
170 Ile Val Cys Val Leu Gly Ile Ser Ala Ile Ile Val Ala Gln Trp Asp
171      245     250     255
172 Arg Phe Ala Thr Pro Lys His Arg Gln Thr Arg Ala Gly Val Phe Leu
173      260     265     270
174 Gly Leu Gly Leu Ser Gly Val Val Pro Thr Met His Phe Thr Ile Ala
175      275     280     285
176 Glu Gly Phe Val Lys Ala Thr Thr Val Gly Gln Met Gly Trp Phe Phe
177      290     295     300
178 Leu Met Ala Val Met Tyr Ile Thr Gly Ala Gly Leu Tyr Ala Ala Arg
179 305     310     315     320
180 Ile Pro Glu Arg Phe Phe Pro Gly Lys Phe Asp Ile Trp Phe Gln Ser

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181          325          330          335
182 His Gln Ile Phe His Val Leu Val Val Ala Ala Ala Phe Val His Phe
183          340          345          350
184 Tyr Gly Val Ser Asn Leu Gln Glu Phe Arg Tyr Gly Leu Glu Gly Gly
185          355          360          365
186 Cys Thr Asp Asp Thr Leu Leu
187          370          375
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191 <211> LENGTH: 900
192 <212> TYPE: DNA
193 <213> ORGANISM: Homo sapiens
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (1)...(897)
199 <400> SEQUENCE: 3
200 atg gaa aaa atg gaa gaa ttt gtt tgt aag gta tgg gaa ggt cgg tgg 48
201 Met Glu Lys Met Glu Glu Phe Val Cys Lys Val Trp Glu Gly Arg Trp
202 1 5 10 15
204 cga gtg atc cct cat gat gta cta cca gac tgg ctc aag gat aat gac 96
205 Arg Val Ile Pro His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp
206 20 25 30
208 ttc ctc ttg cat gga cac cgg cct cct atg cct tct ttc cgg gcc tgt 144
209 Phe Leu Leu His Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys
210 35 40 45
212 ttt aag agc att ttc aga ata cac aca gaa aca ggc aac att tgg aca 192
213 Phe Lys Ser Ile Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr
214 50 55 60
216 cat ctc tta ggt tgt gta ttc ttc ctg tgc ctg ggg atc ttt tat atg 240
217 His Leu Leu Gly Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met
218 65 70 75 80
220 ttt cgc cca aat atc tcc ttt gtg gcc cct ctg caa gag aag gtg gtc 288
221 Phe Arg Pro Asn Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val
222 85 90 95
224 ttt gga tta ttt ttc tta gga gcc att ctc tgc ctt tct ttt tca tgg 336
225 Phe Gly Leu Phe Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp
226 100 105 110
228 ctc ttc cac aca gtc tac tgc cac tca gag ggg gtc tct cgg ctc ttc 384
229 Leu Phe His Thr Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe
230 115 120 125
232 tct aaa ctg gat tac tct ggt att gct ctt ctg att atg gga agt ttt 432
233 Ser Lys Leu Asp Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe
234 130 135 140
236 gtt cct tgg ctt tat tat tct ttc tac tgt aat cca caa cct tgc ttc 480
237 Val Pro Trp Leu Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe
238 145 150 155 160
240 atc tac ttg att gtc atc tgt gtg ctg ggc att gca gcc att ata gtc 528
241 Ile Tyr Leu Ile Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val
242 165 170 175
244 tcc cag tgg gac atg ttt gcc acc cct cag tat cgg gga gta aga gca 576

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245 Ser Gln Trp Asp Met Phe Ala Thr Pro Gln Tyr Arg Gly Val Arg Ala
246      180      185      190
248 gga gtg ttt ttg ggc cta ggc ctg agt gga atc att cct acc ttg cac 624
249 Gly Val Phe Leu Gly Leu Gly Leu Ser Gly Ile Ile Pro Thr Leu His
250      195      200      205
252 tat gtc atc tcg gag ggg ttc ctt aag gcc gcc acc ata ggg cag ata 672
253 Tyr Val Ile Ser Glu Gly Phe Leu Lys Ala Ala Thr Ile Gly Gln Ile
254      210      215      220
256 ggc tgg ttg atg ctg atg gcc agc ctc tac atc aca gga gct gcc ctg 720
257 Gly Trp Leu Met Leu Met Ala Ser Leu Tyr Ile Thr Gly Ala Ala Leu
258 225      230      235      240
260 tat gct gcc cgg atc ccc gaa cgc ttt ttc cct ggc aaa tgt gac atc 768
261 Tyr Ala Ala Arg Ile Pro Glu Arg Phe Phe Pro Gly Lys Cys Asp Ile
262      245      250      255
264 tgg ttt cac tct cat cag ctg ttt cat atc ttt gtg gtt gct gga gct 816
265 Trp Phe His Ser His Gln Leu Phe His Ile Phe Val Val Ala Gly Ala
266      260      265      270
268 ttt gtt cac ttc cat ggt gtc tca aac ctc cag gag ttt cgt ttc atg 864
269 Phe Val His Phe His Gly Val Ser Asn Leu Gln Glu Phe Arg Phe Met
270      275      280      285
272 atc ggc ggg ggc tgc agt gaa gag gat gca ctg tga 900
273 Ile Gly Gly Gly Cys Ser Glu Glu Asp Ala Leu
274      290      295
277 <210> SEQ ID NO: 4
278 <211> LENGTH: 299
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 4
283 Met Glu Lys Met Glu Glu Phe Val Cys Lys Val Trp Glu Gly Arg Trp
284 1      5      10      15
285 Arg Val Ile Pro His Asp Val Leu Pro Asp Trp Leu Lys Asp Asn Asp
286      20      25      30
287 Phe Leu Leu His Gly His Arg Pro Pro Met Pro Ser Phe Arg Ala Cys
288      35      40      45
289 Phe Lys Ser Ile Phe Arg Ile His Thr Glu Thr Gly Asn Ile Trp Thr
290      50      55      60
291 His Leu Leu Gly Cys Val Phe Phe Leu Cys Leu Gly Ile Phe Tyr Met
292 65      70      75      80
293 Phe Arg Pro Asn Ile Ser Phe Val Ala Pro Leu Gln Glu Lys Val Val
294      85      90      95
295 Phe Gly Leu Phe Phe Leu Gly Ala Ile Leu Cys Leu Ser Phe Ser Trp
296      100      105      110
297 Leu Phe His Thr Val Tyr Cys His Ser Glu Gly Val Ser Arg Leu Phe
298      115      120      125
299 Ser Lys Leu Asp Tyr Ser Gly Ile Ala Leu Leu Ile Met Gly Ser Phe
300      130      135      140
301 Val Pro Trp Leu Tyr Tyr Ser Phe Tyr Cys Asn Pro Gln Pro Cys Phe
302 145      150      155      160
303 Ile Tyr Leu Ile Val Ile Cys Val Leu Gly Ile Ala Ala Ile Ile Val

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VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

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